SEQUENCE LISTING

<110> The Regents of the University of California
Whistler, Jennifer L

<120> METHODS AND COMPOSITIONS FOR MODULATING AGONIST-INDUCED
DOWNREGULATION OF G PROTEIN-COUPLED RECEPTORS

<130> 316E-001510US (12101-011-999)

<140> US/10/622,373
<141> 2003-07-18

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<170> PatentIn version 3.1

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Ala Ile Gly Gly Ser Ala Tyr Trp Ala Glu Glu Lys Ser Ser Leu Gly
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Ala Val Ala Arg Glu Glu Ala Lys Pro Glu Ser Glu Glu Glu Ala Ile
         435   440   445
Phe Gly Ser Trp Phe Trp Asp Arg Asp Glu Ala Cys Phe Asp Leu Asn
     450   455   460
Pro Cys Pro Val Tyr Lys Val Ser Asp Arg Phe Arg Asp Ala Ala Glu
465   470   475   480
Glu Leu Asn Ala Ser Ser Arg Pro Gln Thr Trp Asp Glu Val Thr Val
                 485   490   495
Glu Phe Lys Pro Gly Leu Phe His Gly Val Gly Phe Arg Ser Thr Ser
             500   505   510
Pro Phe Gly Ile Pro Glu Glu Ala Ser Glu Met Leu Glu Ala Lys Pro
         515   520   525
Lys Asn Leu Glu Leu Ser Pro Glu Gly Glu Glu Gln Glu Ser Leu Leu
     530   535   540
Gln Pro Asp Gln Pro Ser Pro Glu Phe Thr Phe Gln Tyr Asp Pro Ser
545   550   555   560
Tyr Arg Ser Val Arg Glu Ile Arg Glu His Leu Arg Ala Arg Glu Ser
                 565   570   575
                              Page 7

```
Ala Glu Ser Glu Ser Trp Ser Cys Ser Cys Ile Gln Cys Glu Leu Lys
            580             585             590
Ile Gly Ser Glu Glu Phe Glu Glu Phe Leu Leu Leu Met Asp Lys Ile
            595             600             605
Arg Asp Pro Phe Ile His Glu Ile Ser Lys Ile Ala Met Gly Met Arg
    610             615             620
Ser Ala Ser Gln Phe Thr Arg Asp Phe Ile Arg Asp Ser Gly Val Val
625             630             635             640
Ser Leu Ile Glu Thr Leu Leu Asn Tyr Pro Ser Ser Arg Val Arg Thr
            645             650             655
Ser Phe Leu Glu Asn Met Ile His Met Ala Pro Pro Tyr Pro Asn Leu
            660             665             670
Asn Met Ile Glu Thr Phe Ile Cys Gln Val Cys Glu Glu Thr Leu Ala
            675             680             685
His Ser Val Asp Ser Leu Glu Gln Leu Thr Gly Ile Arg Met Leu Arg
            690             695             700
His Leu Thr Met Thr Ile Asp Tyr His Thr Leu Ile Ala Asn Tyr Met
705             710             715             720
Ser Gly Phe Leu Ser Leu Leu Thr Thr Ala Asn Ala Arg Thr Lys Phe
            725             730             735
His Val Leu Lys Met Leu Leu Asn Leu Ser Glu Asn Pro Ala Val Ala
            740             745             750
Lys Lys Leu Phe Ser Ala Lys Ala Leu Ser Ile Phe Val Gly Leu Phe
            755             760             765
Asn Ile Glu Glu Thr Asn Asp Asn Ile Gln Ile Val Ile Lys Met Phe
    770             775             780
Gln Asn Ile Ser Asn Ile Ile Lys Ser Gly Lys Met Ser Leu Ile Asp
785             790             795             800
Asp Asp Phe Ser Leu Glu Pro Leu Ile Ser Ala Phe Arg Glu Phe Glu
            805             810             815
Glu Leu Ala Lys Gln Leu Gln Ala Gln Ile Asp Asn Gln Asn Asp Pro
            820             825             830
Glu Val Gly Gln Gln Ser
            835
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<210> 7
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> opioid peptide DADLE

<220>
<221> MISC_FEATURE
<222> (2)..(2)
<223> Xaa = D-Ala

<220>
<221> MISC_FEATURE
<222> (5)..(5)
<223> Xaa = D-Leu

<400> 7
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Tyr Xaa Gly Phe Xaa
1               5
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<210> 8
<211> 1491
<212> DNA
<213> Artificial Sequence

<220>
<223> coding sequence for cGASP1 (C-terminal 497 residues of GASP1).

<400> 8
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tcagagactg aagaggaaac catttttggg tcctggttct gggatggaaa agaagtcagt  60
gaagaagcag gaccatgctg tgtatccaag ccagaggatg atgaagagat gattgttgag  120
tcctggttct ggtctagaga caaagccatt aaggaaactg gaactgtggc cacctgtgag  180
tccaagccag aaaatgagga aggggccatt gttgggtctt ggtttgaggc tgaagatgag  240
gtagataaca ggactgacaa tggaagcaac tgtgggtcca ggacattagc tgatgaagat  300
gaggccatag tggggtcctg gttctgggca ggagatgagg cccattttga atcaaatcct  360
agccccgtgt tcagggccat ttgcaggtcc acgtgttcag ttaacagga  gcctgatcct  420
tcacgcaggc ctcagagttg ggaggaggtc actgttcagt tcaagcctgg tccatggggt  480
agggtcggct tcccatctat aagccccttt agatttccga agaggcagc  atctttattc  540
tgtgaaatgt ttggggggcaa acccaggaac atggtactta gcccagaagg ggaagatcag  600
gaatctttgc ttcagcctga tcagcctagt cctgagttcc catttcagta tgatccttcc  660
tacaggtcag tccaggaaat tcgagagcat cttagggcca aggagagtac agagcctgag  720
agttcatcct gtaactgcat acaatgtgag ctgaaaattg gttctgaaga gtttgaagaa  780
ctcctttttat taatggaaaa aattcgggat cctttttattc atgaaaatatc taaaatcgca  840
atgggtatga gaagtgcttc tcaatttacc cgagatttca ttcgagattc aggtgttgtc  900
tcacttattg aaaccttgct taattatccg tcctcccgag ttagaacaag tttttttggaa  960
aatatgattc gcatggcccc accttatccg aatctaaaca taattcagac atacatatgt  1020
aaagtgtgtg aggaaaccct tgcttatagc gtggattccc cggaacagct gtctggaata  1080
aggatgatta gacatctcac tactactact gactatcaca cactggttgc caattatatg  1140
tctgggtttc tctccttatt agctacaggc aatgccaaaa caaggtttca tgttttgaaa  1200
atgctactga atttgtctga aaatcttttc atgacaaaag aactactcag tgctgaagca  1260
gtgtcagaat ttataggcct cttttaacagg gaagagacaa atgacaatat tcaaattgtt  1320
cttgcaatat ttgagaatat tggcaacaat atcaaaaaag aaacagtgtt ctctgatgat  1380
gatttcaata ttgagccgct tatttctgca ttccacaaag ttgagaaatt tgctaaggaa  1440
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<210> 9
<211> 497
<212> PRT
<213> Artificial Sequence

<220>
<223> cGASP1 (C-terminal 497 residues of GASP1)

<400> 9
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Ser Glu Thr Glu Glu Glu Thr Ile Phe Gly Ser Trp Phe Trp Asp Gly
 1               5                  10                 15
Lys Glu Val Ser Glu Glu Ala Gly Pro Cys Cys Val Ser Lys Pro Glu
            20                  25                  30
Asp Asp Glu Glu Met Ile Val Glu Ser Trp Phe Trp Ser Arg Asp Lys
            35                  40                  45
Ala Ile Lys Glu Thr Gly Thr Val Ala Thr Cys Glu Ser Lys Pro Glu
    50                  55                  60
Asn Glu Glu Gly Ala Ile Val Gly Ser Trp Phe Glu Ala Glu Asp Glu
65                  70                  75                  80
Val Asp Asn Arg Thr Asp Asn Gly Ser Asn Cys Gly Ser Arg Thr Leu
            85                  90                  95
Ala Asp Glu Asp Glu Ala Ile Val Gly Ser Trp Phe Trp Ala Gly Asp
            100                 105                 110
Glu Ala His Phe Glu Ser Asn Pro Ser Pro Val Phe Arg Ala Ile Cys
            115                 120                 125
Arg Ser Thr Cys Ser Val Glu Gln Glu Pro Asp Pro Ser Arg Arg Pro
    130                 135                 140
Gln Ser Trp Glu Glu Val Thr Val Gln Phe Lys Pro Gly Pro Trp Gly
145                 150                 155                 160
Arg Val Gly Phe Pro Ser Ile Ser Pro Phe Arg Phe Pro Lys Glu Ala
                165                 170                 175
Ala Ser Leu Phe Cys Glu Met Phe Gly Gly Lys Pro Arg Asn Met Val
            180                 185                 190
```

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Leu Ser Pro Glu Gly Glu Asp Gln Glu Ser Leu Leu Gln Pro Asp Gln
    195             200               205
Pro Ser Pro Glu Phe Pro Phe Gln Tyr Asp Pro Ser Tyr Arg Ser Val
    210             215               220
Gln Glu Ile Arg Glu His Leu Arg Ala Lys Glu Ser Thr Glu Pro Glu
225             230               235               240
Ser Ser Ser Cys Asn Cys Ile Gln Cys Glu Leu Lys Ile Gly Ser Glu
            245               250               255
Glu Phe Glu Glu Leu Leu Leu Leu Met Glu Lys Ile Arg Asp Pro Phe
        260               265               270
Ile His Glu Ile Ser Lys Ile Ala Met Gly Met Arg Ser Ala Ser Gln
    275               280               285
Phe Thr Arg Asp Phe Ile Arg Asp Ser Gly Val Val Ser Leu Ile Glu
    290               295               300
Thr Leu Leu Asn Tyr Pro Ser Ser Arg Val Arg Thr Ser Phe Leu Glu
305             310               315               320
Asn Met Ile Arg Met Ala Pro Pro Tyr Pro Asn Leu Asn Ile Ile Gln
            325               330               335
Thr Tyr Ile Cys Lys Val Cys Glu Glu Thr Leu Ala Tyr Ser Val Asp
            340               345               350
Ser Pro Glu Gln Leu Ser Gly Ile Arg Met Ile Arg His Leu Thr Thr
    355               360               365
Thr Thr Asp Tyr His Thr Leu Val Ala Asn Tyr Met Ser Gly Phe Leu
    370               375               380
Ser Leu Leu Ala Thr Gly Asn Ala Lys Thr Arg Phe His Val Leu Lys
385             390               395               400
Met Leu Leu Asn Leu Ser Glu Asn Leu Phe Met Thr Lys Glu Leu Leu
            405               410               415
Ser Ala Glu Ala Val Ser Glu Phe Ile Gly Leu Phe Asn Arg Glu Glu
            420               425               430
Thr Asn Asp Asn Ile Gln Ile Val Leu Ala Ile Phe Glu Asn Ile Gly
            435               440               445
Asn Asn Ile Lys Lys Glu Thr Val Phe Ser Asp Asp Asp Phe Asn Ile
    450               455               460
Glu Pro Leu Ile Ser Ala Phe His Lys Val Glu Lys Phe Ala Lys Glu
465               470               475               480
Leu Gln Gly Lys Thr Asp Asn Gln Asn Asp Pro Glu Gly Asp Gln Glu
            485               490               495
Asn
```